

## SEQUENCE LISTING

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 HOET, RENE

<120> NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS

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<140> 09/837,306

<141> 2001-04-17

<150> 60/198,069

<151> 2000-04-17

<160> 428

<170> PatentIn Ver. 2.1

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Lys Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr
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Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn 85 90 95

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp 100 105 110

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Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser 130 135 140

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr 145 150 155 160

Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro 165 170 175

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val 180 185 190

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser 195 200 205

Ser Val Val Thr Val Pro Ser Ser Leu Gly Thr Gln Thr Tyr Ile 210 215 220

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Glu Pro Lys Ser Cys Ala Ala Ala His His His His His Ser Ala 245 250 255

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala Asp Ile 260 265 270

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Leu Ala Lys Pro His Thr Glu Ile Ser Phe Thr Asn Val Trp Lys Asp 290 295 300

Asp Lys Thr Leu Asp Arg Tyr Ala Asn Tyr Glu Gly Cys Leu Trp Asn

305 310 315 320

Ala Thr Gly Val Val Cys Thr Gly Asp Glu Thr Gln Cys Tyr Gly 325 330 335

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Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp 50 55 60

Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn 65 70 75 80

Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln 85 90 95

Ser Val Glu Cys Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu 100 105 110

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Val Gly Arg Phe Ala Lys Thr Pro Arg Val Leu Arg Ile Pro Asp Lys 35 40 45

Pro Ser Ile Ser Asp Leu Leu Ala Ile Gly Arg Gly Asn Asp Ser Tyr
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Phe Asn Thr Arg Ser Trp Asn Asp Lys Glu Arg Gln Pro Ile Ile Asp 85 90 95

Trp Phe Leu His Ala Arg Lys Leu Gly Trp Asp Ile Ile Phe Leu Val

Gln Asp Leu Ser Ile Val Asp Lys Gln Ala Arg Ser Ala Leu Ala Glu 115 120 125

His Val Val Tyr Cys Arg Arg Leu Asp Arg Ile Thr Leu Pro Phe Val 130 135 140

Gly Thr Leu Tyr Ser Leu Ile Thr Gly Ser Lys Met Pro Leu Pro Lys 145 150 155 160

Leu His Val Gly Val Val Lys Tyr Gly Asp Ser Gln Leu Ser Pro Thr 165 170 175

Val Glu Arg Trp Leu Tyr Thr Gly Lys Asn Leu Tyr Asn Ala Tyr Asp 180 185 190

Thr Lys Gln Ala Phe Ser Ser Asn Tyr Asp Ser Gly Val Tyr Ser Tyr 195 200 205

Leu Thr Pro Tyr Leu Ser His Gly Arg Tyr Phe Lys Pro Leu Asn Leu 210 215 220

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## oligonucleotide

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cagaaacctg gccaggttcc caggetcctc atctatggtg catccaccag ggccactgat 180
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aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg 480
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Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr Asp Ile Pro Ala Arg
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg
Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Arg Tyr Gly Ser
Ser Pro Gly Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
                            120
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
    130
                        135
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
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145
                    150
                                        155
                                                             160
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                165
                                    170
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
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His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
Val Thr Lys Ser Phe Asn Lys Gly Glu Cys Lys Gly Glu Phe Ala
<210> 306
<211> 700
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agagecacce tetectgeag ggecagteag gtgteteeag gggaaagage caccetetee 120
tgcaatcttc tcagcaactt agcctggtac cagcagaaac ctggccaggc tcccaggctc 180
ctcatctatg gtgcttccac cggggccatt ggtatcccag ccaggttcag tggcagtggg 240
tetgggacag agtteactet caccateage ageetgeagt etgaagattt tgeagtgtat 300
ttctgtcagc agtatggtac ctcaccgccc actttcggcg gagggaccaa ggtggagatc 360
aaacgaactg tggctgcacc atctgtcttc atcttcccgc catctgatga gcagttgaaa 420
tctggaactg cctctgttgt gtgcccgctg aataacttct atcccagaga ggccaaagta 480
cagtggaagg tggataacgc cctccaatcg ggtaactccc aggagagtgt cacagagcag 540
gacaacaagg acagcaccta cagcctcagc agcaccctga cgctgagcaa agtagactac 600
gagaaacacg aagtctacgc ctgcgaagtc acccatcagg gccttagctc gcccgtcacg 660
aagagcttca acaggggaga gtgtaagaaa gaattcgttt
<210> 307
<211> 222
<212> PRT
<213> Unknown Organism
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<400> 307
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Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asn Leu
Leu Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arq
Leu Leu Ile Tyr Gly Ala Ser Thr Gly Ala Ile Gly Ile Pro Ala Arg
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Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser

Leu Gln Ser Glu Asp Phe Ala Val Tyr Phe Cys Gln Gln Tyr Gly Thr 90 Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr 105 Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Pro Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly 155 Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Asn Lys Asp Ser Thr Tyr 165 175 Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Val Asp Tyr Glu Lys His 185 Glu Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val 200 205 Thr Lys Ser Phe Asn Arg Gly Glu Cys Lys Lys Glu Phe Val 210 215 <210> 308 <211> 45 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Synthetic oligonucleotide gctgtgtatt actgtgcgag cacatccgtg ttgttcacgg atgtg 45 <210> 309 <211> 45 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Synthetic oligonucleotide <400> 309 gccgtgtatt actgtgcgag cacatccgtg ttgttcacgg atgtg

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  <212> DNA
  <213> Artificial Sequence
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  <400> 310
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  <210> 311
  <211> 45
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  <400> 311
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  <211> 45
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  tagagttgtc tctagactta gtgaagcg
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<210> 315
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                                                                    44
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<211> 44
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## oligonucleotide

<400> 318 cacateegtg ttgtteaegg atgtgggaga gtggagaetg agte	44
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<211> 70
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oligonucleotide	
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<211> 22
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<400> 350
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caaaccagtc gtcaggatct taacctgagg ctttttttac ctactctgca agcagcgaca 180
tctggtttga cacagagcga tccgcgtcgt cagttggtag aaacattaac acgttgggat 240
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aacgtttggc tgaccagtat gttgaagcgt accgtagtgg ctgccgtacc tatgccattt 360
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ccacaggegg ttgatetgtt tgetgggaaa ccacageagg aggttgtgtt ggetgegetg 540
gaagatacct gggagactct ttccaaacgc tatggcaata atgtgagtaa ctggaaaaca 600
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gaagaaacgc gtcatcaggc ggagtatcaa aaccgtggaa cagaaaacga tatgattgtt 720
ttctcaccaa cgacaagcga tcgtcctgtg cttgcctggg atgtggtcgc acccggtcag 780
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<211> 286

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<213> Unknown Organism

<220>

<223> Description of Unknown Organism: pCES5

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Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys 20 25 30

Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp 35 40 45

Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe 50 55 60

Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser 65 70 75 80

Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser 85 90 95

Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr 100 105 110

Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser 115 120 125

Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys 130 135 140

Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu 145 150 155 160

Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg 165 170 175

Asp Thr Thr Met Pro Val Ala Met Ala Thr Thr Leu Arg Lys Leu Leu 180 185 190

Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp

195 200 205

Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro 210 215 220

Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser 225 230 235 240

Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile
245 250 255

Val Val Ile Tyr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn 260 265 270

Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp
275 280 285

<210> 355

<211> 138

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: pCES5

<400> 355

Met Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr Ser 1 5 10 15

His Ser Ala Gln Val Gln Leu Gln Val Asp Leu Glu Ile Lys Arg Gly
20 25 30

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln 35 40 45

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr 50 55 60

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser 65 70 75 80

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr 85 90 95

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
100 105 110

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro 115 120 125

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys 130 135

<210> 356

<211> 48

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<212> PRT
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<213> Unknown Organism

<220>

<223> Description of Unknown Organism: pCES5

<400> 356

Met Lys Tyr Leu Leu Pro Thr Ala Ala Gly Leu Leu Leu Leu Ala 1 5 10 15

Ala Gln Pro Ala Met Ala Glu Val Gln Leu Leu Glu Ser Gly Gly Gly 20 25 30

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
35 40 45

<210> 357

<211> 28

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: pCES5

<400> 357

Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu 1 5 10 15

Ser Leu Ser Ile Arg Ser Gly Gln His Ser Pro Thr

<210> 358

<211> 129

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: pCES5

<400> 358

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys

1 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr 20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser 35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser 50 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr 65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys

85 90 95

Lys Val Glu Pro Lys Ser Cys Ala Ala Ala His His His His His His 100 105 110

Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala 115 120 125

Ala

<210> 359

<211> 404

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: pCES5

<400> 359

Thr Val Glu Ser Cys Leu Ala Lys Pro His Thr Glu Asn Ser Phe Thr
1 5 10 15

Asn Val Trp Lys Asp Asp Lys Thr Leu Asp Arg Tyr Ala Asn Tyr Glu 20 25 30

Gly Cys Leu Trp Asn Ala Thr Gly Val Val Cys Thr Gly Asp Glu 35 40 45

Thr Gln Cys Tyr Gly Thr Trp Val Pro Ile Gly Leu Ala Ile Pro Glu
50 60

Asn Glu Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly Ser 65 70 75 80

Glu Gly Gly Gly Thr Lys Pro Pro Glu Tyr Gly Asp Thr Pro Ile Pro 85 90 95

Gly Tyr Thr Tyr Ile Asn Pro Leu Asp Gly Thr Tyr Pro Pro Gly Thr 100 105 110

Glu Gln Asn Pro Ala Asn Pro Asn Pro Ser Leu Glu Glu Ser Gln Pro 115 120 125

Leu Asn Thr Phe Met Phe Gln Asn Asn Arg Phe Arg Asn Arg Gln Gly 130 135 140

Ala Leu Thr Val Tyr Thr Gly Thr Val Thr Gln Gly Thr Asp Pro Val
145 150 155 160

Lys Thr Tyr Tyr Gln Tyr Thr Pro Val Ser Ser Lys Ala Met Tyr Asp 165 170 175

Ala Tyr Trp Asn Gly Lys Phe Arg Asp Cys Ala Phe His Ser Gly Phe 180 185 190

Asn Glu Asp Pro Phe Val Cys Glu Tyr Gln Gly Gln Ser Ser Asp Leu 195 200 205 Pro Gln Pro Pro Val Asn Ala Gly Gly Gly Ser Gly Gly Gly Ser Gly 210 215 220

Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly 225 230 235 240

Gly Ser Glu Gly Gly Gly Ser Gly Gly Ser Gly Ser Gly Asp Phe
245 250 255

Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn 260 265 270

Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser 275 280 285

Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val 290 295 300

Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser 305 310 315 320

Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met 325 330 335

Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys 340 345 350

Arg Pro Tyr Val Phe Gly Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp 355 360 365

Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr 370 375 380

Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg 385 390 395 400

Asn Lys Glu Ser

<210> 360

<211> 69

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Kappa FR1 GLGs

<400> 360

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60 atcacttgc

<210> 361

<211> 69

<212> DNA

<213> Unknown Organism

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atcacttgc
<210> 362
<211> 69
<212> DNA
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<223> Description of Unknown Organism: Kappa FR1 GLGs
<400> 362
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgc
<210> 363
<211> 69
<212> DNA
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gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgc
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<211> 69
<212> DNA
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atcacttgc
<210> 365
<211> 69
<212> DNA
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<400> 365
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atcacttgt
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<210> 366
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<400> 366
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<211> 69
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atcacttgt
<210> 368
<211> 69
<212> DNA
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atcacttgc
<210> 369
<211> 69
<212> DNA
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<400> 369
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atcacttgc
<210> 370
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<211> 69

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  atcacttgt
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  <211> 69
  <212> DNA
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  <400> 371
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  atcacttgt
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··· <211> 69
  <212> DNA
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  <400> 372
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  atcacttgc
  <210> 373
  <211> 69
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  <400> 373
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  atcacttgc
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  <210> 374
  <211> 69
  <212> DNA
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atcacttgt
<210> 375
<211> 69
<212> DNA
<213> Unknown Organism
<220>
<223> Description of Unknown Organism: Kappa FR1 GLGs
<400> 375
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atcagttgt
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<210> 376
<211> 69
<212> DNA
<213> Unknown Organism
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<400> 376
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atcacttgc
<210> 377
<211> 69
<212> DNA
<213> Unknown Organism
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atcacttgc
<210> 378
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<400> 378
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atctcctgc
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atctcctgc
<210> 380
<211> 69
<212> DNA
<213> Unknown Organism
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<400> 380
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atctcctgc
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<211> 69
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<211> 69
<212> DNA
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<223> Description of Unknown Organism: Kappa FR1 GLGs
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<210> 383
<211> 69
<212> DNA
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<223> Description of Unknown Organism: Kappa FR1 GLGs
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tcctgc
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<212> DNA
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acctgc
<210> 422
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acctgc
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<210> 424
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